

## **Supplemental Information**

**Supplemental Figure S1** Direct immunofluorescence microscopy showing the transfection efficiency of EGFP-Src (Src) and Cherry-FRB (FRB), serving as input control for Fig. 1c.

**Supplemental Figure S2 (a)** Exogenous co-immunoprecipitation studies in HEK293 cells show that activation of Src-iFKBP (Src\*) increases the interaction of Myc-synaptopodin (Synpo-WT) with FLAG-calcineurin A (FLAG-CnA) when compared with inactive Src-iFKBP (Src). Alanine substitution of Y29 (Synpo-Y29A) or Y344 (Synpo-Y344A) does not interfere with calcineurin binding at baseline (Src) or activation of Src (Src\*). No interaction is found with the negative control Myc-Raver. In the FLAG eluate, FLAG-CnA is marked by an arrow, the other bands represent heavy (\*) and light chain (\*\*) of the anti-FLAG antibody that was used to precipitate FLAG-CnA. Molecular weight markers are in kDa. **(b)** Direct immunofluorescence microscopy showing the transfection efficiency of EGFP-Src (Src) and Cherry-FRB (FRB).

**Supplemental Figure S3** Exogenous co-immunoprecipitation studies in HEK293 show that Src inhibitor 1 (SrcI-1) lowers the basal interaction between FLAG-calcineurin and Myc-synaptopodin. No interaction is found with the negative control Myc-Raver.

**Supplemental Figure S4 (a)** Immunofluorescence of EGFP-Src and Cherry-FRB shows near complete infection/expression efficiency in podocytes; scale bar 20  $\mu\text{m}$ . **(b)** The calcineurin inhibitor CsA does not restore stress fibres in synaptopodin-depleted (synpo shRNA) cells in the presence of activated Src (Src\*); scale bar 20  $\mu\text{m}$ .

**Supplemental Figure S5** (a) Phalloidin labelling reveals well-developed stress fibres in non-infected control podocytes before (left) and after rapamycin treatment (middle) and in Src-iFKB/FRB co-infected podocytes (right); scale bar 20  $\mu$ m. (b) Synaptopodin protein abundance is comparable between control (con) and rapamycin (rapa) treated podocytes. GAPDH serves as a loading control. (c) Protein abundance of active pSrc (Y416), inactive pSrc (Y527) and total Src is comparable between control (con) and rapamycin (rapa) treated podocytes. Molecular weight markers are in kDa. (d) Western blot analysis shows the degree of protein depletion in podocytes expressing shRNAs that target synaptopodin (Synpo), Vav2 or Rac1. GAPDH serves as a loading control.

**Supplemental Figure S6** The Rac1 inhibitor NSC23766SF restores stress fibres in synaptopodin-depleted (synpo shRNA) cells; scale bar 20  $\mu$ m.

**Supplemental Figure S7** Lck mRNA expression is readily detected in spleen (positive control) but is absent from isolated mouse kidney glomeruli (glom), undifferentiated (undiff) or differentiated (diff) podocytes. In contrast, c-Src expression is found in glomeruli, undifferentiated and differentiated podocytes and in spleen. GAPDH serves as loading control.

**Supplemental Figure S8** As a control experiment, phalloidin labelling reveals that overexpression of four different GFP-synaptopodin constructs has no effect on stress fibres in podocytes prior to PS treatment; scale bar 20  $\mu$ m.

**Supplemental Figure S9** As a control experiment, phalloidin labelling reveals that two independent shRNAs for synpo (#3 and #4) have the same effect on disrupting stress fibres in podocytes, which is rescued by the Rac1 inhibitor NSC27366; scale bar 20  $\mu$ m.

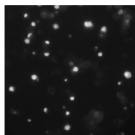
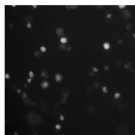
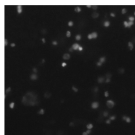
**Supplemental Table S1 Sequences of shRNAs used for gene silencing experiments**

<b>shRNA</b>	<b>Sequence</b>
VAV2 1	CCGGAAGTGGAGGAGTGCACACTCACTCGAGTGAGTGTGCACTCCTCCACTT TTTTTG
VAV2 2	CCGGAAGGAATGCCTGGAGGTGATCCTCGAGGATCACCTCCAGGCATTCTT TTTTTG
p190RhoGAP1	CCGGCGGTACATTAGAGATGCACATCTCGAGATGTGCATCTCTAATGTACCGT TTTTG
p190RhoGAP2	CCGGCGGTTGGTTCATGGGTACATTCTCGAGAATGTACCCATGAACCAACCGT TTTTG
Rac1	CCGGCGCAGACAGACGTGTTCTTAACCTCGAGTTAAGAACACGTCTGTCTGCGT TTTTG

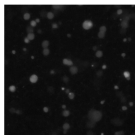
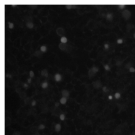
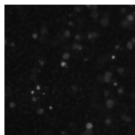
**Supplemental Table S2 Sequences of RT PCR primers for mRNA Src kinase detection**

<b>Primer</b>	
Src Forward	CGGCTGCAGATTGTCAATAA
Src Reverse	AGGCTTGGATGTGGGACATA
Lck Forward	ATTACATCCATCGGGACCTG
Lck Reverse	CATCCAGAACACTCCGAAGG
GAPDH Forward	CTGCACCACCAACTGCTTAGC
GAPDH Reverse	GGCATGGACTGTGGTCATGAG

FLAG-CnA



Src



FRB

Synpo WT

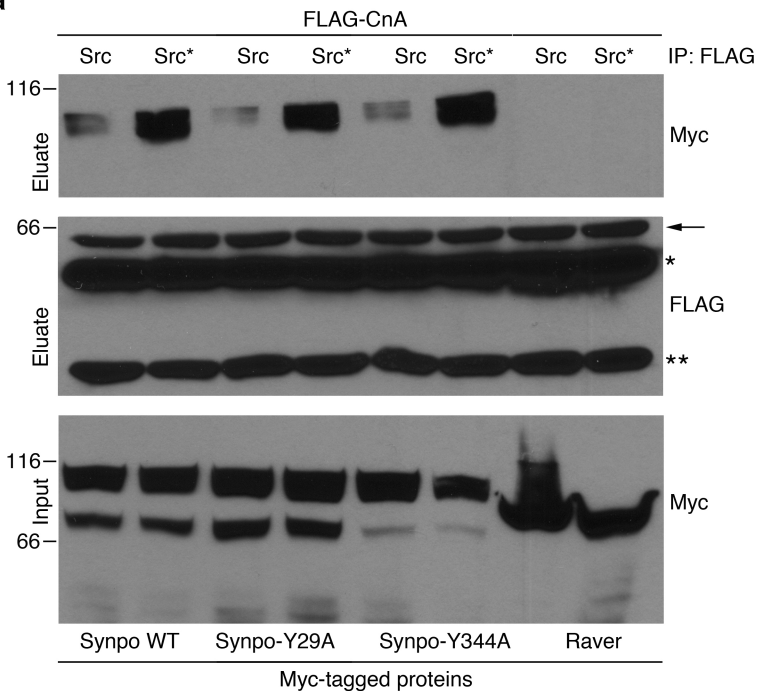
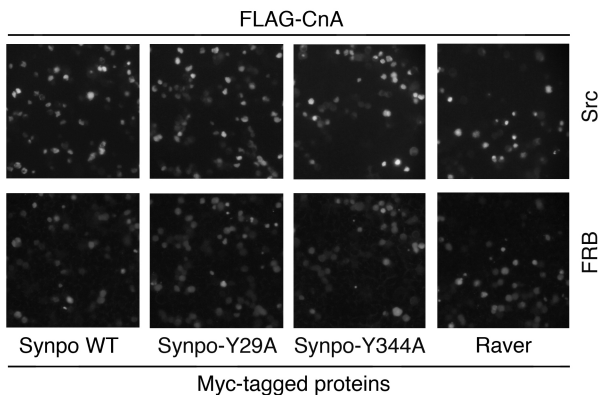
Synpo-Y222A

Raver

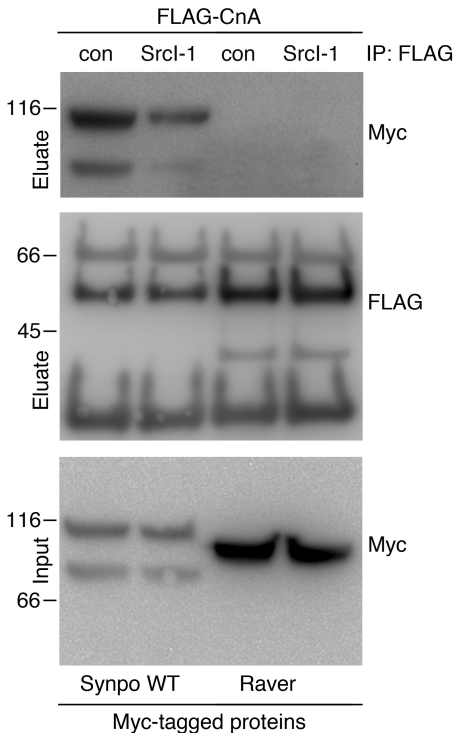
Myc-tagged proteins

Supplemental Figure S1



**a****b**

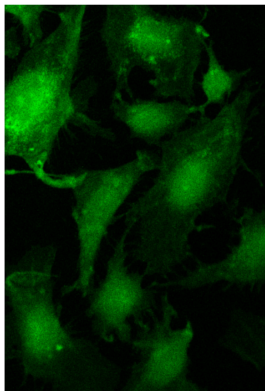
Supplemental Figure S2



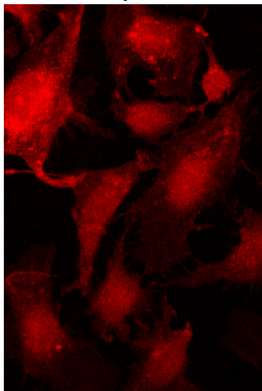
Supplemental Figure S3

**a**

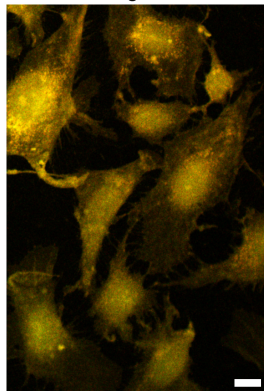
EGFP-Src



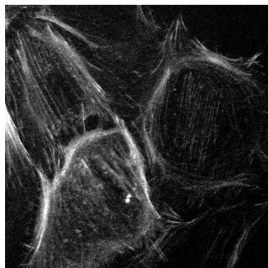
Cherry-FRB



merge

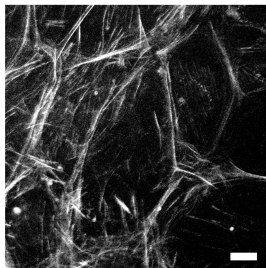
**b**

synpo shRNA + src\*



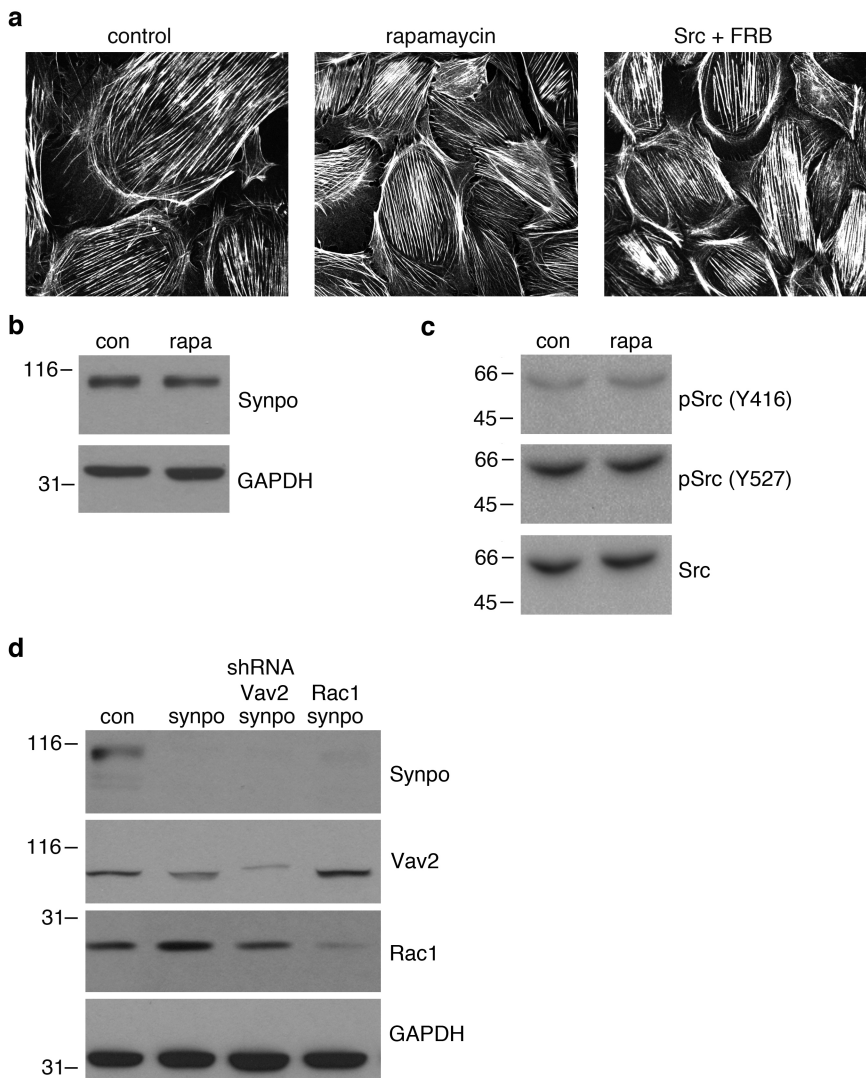
control

synpo shRNA + src\*



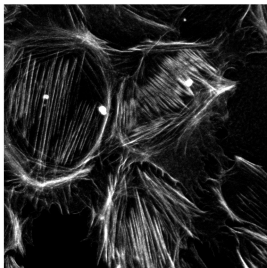
CsA

Supplemental Figure S4

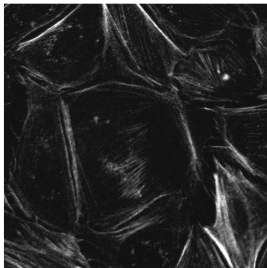


Supplemental Figure S5

control shRNA



synpo shRNA

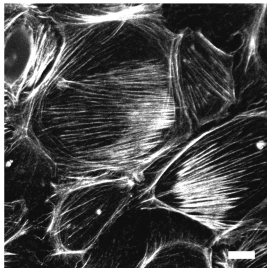
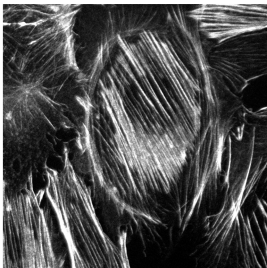


control

control

control shRNA

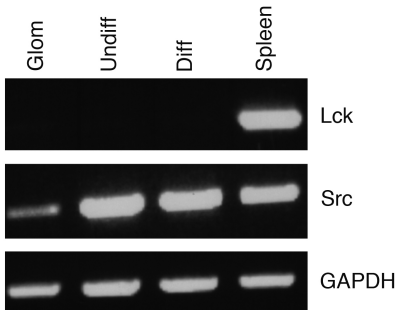
synpo shRNA



control

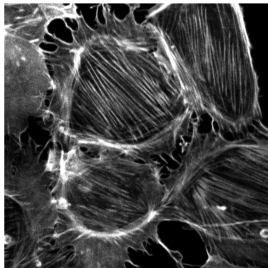
NSC27366

Supplemental Figure S6

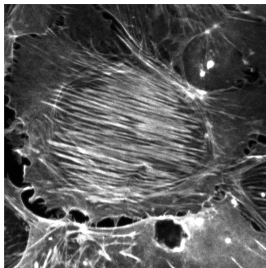


Supplemental Figure S7

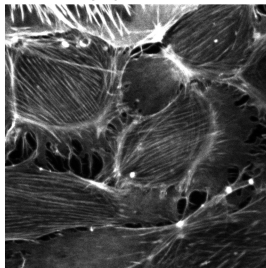
Synpo-WT



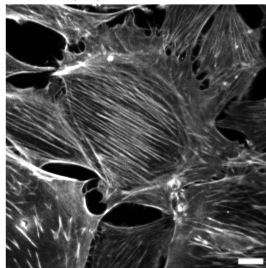
Synpo-Y222A



Synpo-ED



Synpo-CM1+2

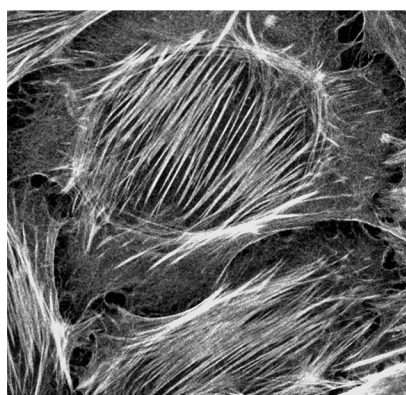
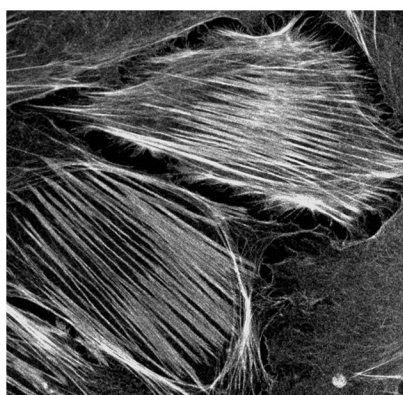


Supplemental Figure S8

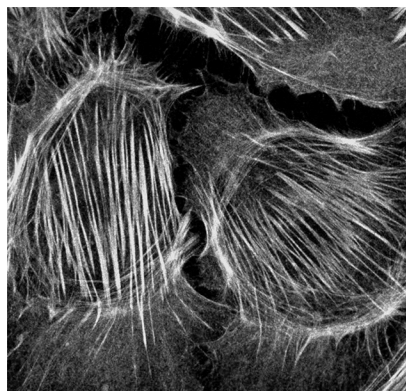
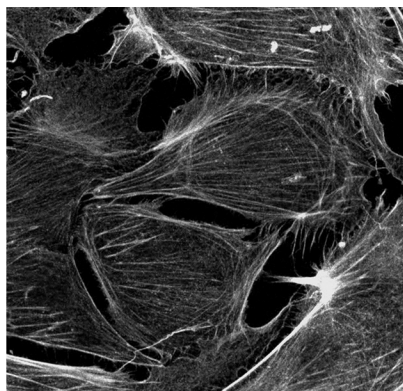
**PBS**

**NSC27366**

**control  
shRNA**



**synpo  
shRNA #3**



**synpo  
shRNA #4**

